

ABSTRACT

An apparatus, method, etc. that in designing of the base sequence of, for example, siRNA, realize high-speed retrieval any genes containing analogous base sequences without omission.

- 5 Accordingly, retrieval is carried out in such a manner that two partial sequences of given length and any extra part are identified from inputted base sequences, and that hamming distance being the number of corresponding bases incompatible with each other is divided and assigned to the partial sequences and extra part and out of the two partial sequences, one with an assigned number not greater is selected and retrieved.